In the Specification:

Please amend the specification as shown:

Please delete the paragraph [0012] and replace it with the following amended paragraph:

Figure 2 shows a polypeptide sequence **(SEQ ID NO: 2)** encoded by the nucleic acid of SEQ. ID. NO: 1

Please delete the paragraph [0015] and replace it with the following amended paragraph:

Figure 5A shows a nucleotide sequence alignment for human PLA2G1B **(SEQ ID NO: 3)** and related sequences from mouse **(SEQ ID NO: 4)**, rat **(SEQ ID NO: 5)**, and *P. obesus* (sand rat) **(SEQ ID NO: 6)**. Figure 5B shows an amino acid sequence alignment between human PLA2G1B and related sequences from mouse, rat, and *P. obesus*. The human PLA2G1B amino acid sequence **(SEQ ID NO: 7)** in Figure 5B has 148 amino acids and the mouse **(SEQ ID NO: 8)**, rat **(SEQ ID NO: 9)**, and *P. obesus* **(SEQ ID NO: 10)** sequences have 146 amino acids. The human PLA2G1B amino acid sequence is 78% identical to the mouse sequence, 76% identical to the rat sequence, and 76% identical to the *P. obesus* sequence. The mouse sequence is 88% identical to the rat sequence and 77% identical to the *P. obesus* sequence, and the rat sequence is 80% identical to the *P. obesus* sequence.

Please delete the paragraph [00123] and replace it with the following amended paragraph:

When designing the siRNA molecules, the targeted region often is selected from a given DNA sequence beginning 50 to 100 nt downstream of the start codon. *See, e.g.*, Elbashir *et al,. Methods 26*:199-213 (2002). Initially, 5' or 3' UTRs and regions nearby the start codon were avoided assuming that UTR-binding proteins and/or translation initiation complexes may interfere with binding of the siRNP or RISC endonuclease complex. Sometimes regions of the target 23 nucleotides in length conforming to the sequence motif AA(N19)TT (N, an nucleotide) **(SEQ ID NO: 79)**, and regions with approximately 30% to 70% G/C-content (often about 50% G/C-content) often are selected. If no suitable

sequences are found, the search often is extended using the motif NA(N21). The sequence of the sense siRNA sometimes corresponds to (N19) TT or N21 (position 3 to 23 of the 23-nt motif), respectively. In the latter case, the 3' end of the sense siRNA often is converted to TT. The rationale for this sequence conversion is to generate a symmetric duplex with respect to the sequence composition of the sense and antisense 3' overhangs. The antisense siRNA is synthesized as the complement to position 1 to 21 of the 23-nt motif. Because position 1 of the 23-nt motif is not recognized sequence-specifically by the antisense siRNA, the 3'-most nucleotide residue of the antisense siRNA can be chosen deliberately. However, the penultimate nucleotide of the antisense siRNA (complementary to position 2 of the 23-nt motif) often is complementary to the targeted sequence. For simplifying chemical synthesis, TT often is utilized. siRNAs corresponding to the target motif NAR(N17)YNN, where R is purine (A,G) and Y is pyrimidine (C,U), often are selected. Respective 21 nucleotide sense and antisense siRNAs often begin with a purine nucleotide and can also be expressed from pol III expression vectors without a change in targeting site. Expression of RNAs from pol III promoters often is efficient when the first transcribed nucleotide is a purine.

Please delete Table #2 on page 45 and replace it with the following amended Table:

Table 2

Reference SNP ID	Position in SEQ ID NO:1	First PCR primer	SEQ ID NO:	Second PCR primer	SEQ ID NO:
rs2009391	4050	TGCAGAGGCTCAATCACTGT	**11**	CAGGTGTGGTGGTGGATTG	**12**
rs5631	4689	CACAGGCCACAGCAAACAG	**13**	TCAGACTTGCAGGTTGAAAAAG	**14**
rs5632	6282	GGCAGACCGATTTGAACTCT	**15**	CGGGATCACGCACTTGA	**16**
rs5633	6358	GGCAGTTCCGCAAAATGAT	**17**	TGCAGGCGGATCACTTACTT	**18**
rs5634	7256	AGCTGTCCCTCCCACTTTC	**19**	GTGTGGGTGTACGGGTTGT	**20**
rs5635	7300	AGCTGTCCCTCCCACTTTC	**21**	ATAGGTCAAGGAAGGGATAAAC	**22**
rs5636	7301	AGCTGTCCCTCCCACTTTC	**23**	ATAGGTCAAGGAAGGGATAAAC	**24**
rs5637	7328	CAAGAAGCTGGACAGCTGTA	**25**	ATAGGTCAAGGAAGGGATAAAC	**26**
rs1186217	8062	ATCACCTCAACCTCCG	**27**	GGTGGTGCACGCTTGTA	**28**

Reference SNP ID	Position in SEQ ID NO:1	First PCR primer	SEQ ID NO:	Second PCR primer	SEQ ID NO:
		TTCA		ATT	
rs1179387	9182	AAGGTAAGCAGAGAT ACGTAAATTAT	**29**	GGTTATCTTTGGGTAGT AGGATTATA	**30**

Please delete Table #3 on pages 45-46 and replace it with the following amended Table:

Table 3

Position in SEQ ID NO:1	Extension Oligonucleotide
4050	TGAGATGGGAGGATCT (antisense) **(SEQ ID NO: 31)**
4689	ACTGGGAACCTCGA (antisense) **(SEQ ID NO: 32)**
6282	GCTGATGCCGCTG (antisense) **(SEQ ID NO: 33)**
6358	GGAGTGACCCCTT **(SEQ ID NO: 34)**
7256	ACACATGACAACTGCTA **(SEQ ID NO: 35)**
7300	GGTGTGGGTGTACGG (antisense) **(SEQ ID NO: 36)**
7301	GGTGTGGGTGTACGG (antisense) **(SEQ ID NO: 37)**
7328	CCACACCTATTCATACTC **(SEQ ID NO: 38)**
8062	CTTAGGCAGGAGAATC (antisense) **(SEQ ID NO: 39)**
9182	GTAATGCAACTTCAAAC **(SEQ ID NO: 40)**

Please delete Table #4 on page 47 and replace it with the following amended Table:

Table 4

Reference SNP ID	Position in SEQ ID NO:1	First PCR primer	SEQ ID NO:	Second PCR primer	SEQ ID NO:
rs2701632	436	ACCCACTTAGCATCCT TCAG	**41**	TCTTATGTGGGTTCC TTGGG	**42**
rs2701631	839	TGTGGCCATTGTGACT GAGA	**43**	GCCCGGGTGACAGA GTG	**44**
rs5633	6358	TGTGGCAGTTCCGCAA AATG	**45**	AGTAGCAGCCGTAGT TGTTG	**46**
rs2070873	6653	ACCCCGTTAGAGATGG AAAC	**47**	CTGTTGCTACATTCT GCCAC	**48**
rs5637	7328	AATTTCTGCTGGACAA CCCG	**49**	CCTACTGCTACAGGT GATTG	**50**
rs1179387	9182	CAAGCCAAAAGTAATG	**51**	GGATTATAGATGCCT	**52**

Reference SNP ID	Position in SEQ ID NO:1	First PCR primer	SEQ ID NO:	Second PCR primer	SEQ ID NO:
		CAAC		TCCAC	
rs2066539	10164	TCATCTCACACTGTAC TCTC	**53**	CAATATCCAAACATG AGGTC	**54**
rs2701629	11649	GACAGAGAGAGACAC TATCT	**55**	GAAATGCAAGCTGTT ATTGG	**56**

Please delete Table #5 on pages 47-48 and replace it with the following amended Table

Table 5

Position in SEQ ID NO:1	Extend Probe	SEQ ID NO:	Termination Mix
436	TTAGCATCCTTCAGGCCTAAA	**57**	A,C,G
839	GACTCTGCCTCAAAATAAATAAAA (antisense)	**58**	C,G,T
6358	GCCGTAGTTGTTGTATTCCAA (antisense)	**59**	A,C,T
6653	GTGCAAAACAGTGGGCGATGCT	**60**	A,C,T
7328	TGATTGCCGAGCCAGAGCA (antisense)	**61**	A,C,G
9182	TTTCCATAATAGATATTTATGTAG (antisense)	**62**	C,G,T
10164	CACTGTACTCTCCAATAAAGCACC	**63**	A,C,G
11649	CAAACAAACACACACACAAAAC	**64**	C,G,T

Please delete the paragraph[00171] and replace it with the following amended paragraph:

The SNP at position 7256 of SEQ ID NO: 1 was also allelotyped and genotyped in NIDDM and non-NIDDM patients from the pool described above (see Example 4). The following PCR primers were used: ACGTTGGATGGGGTTGTCCAGCAGAAATTTAC (forward PCR primer) **(SEQ ID NO: 65)** and ACGTTGGATGCTTTCCAGGTGCTGCCAG (reverse PCR primer) **(SEQ ID NO: 66)**; and AGACACATGACAACTGCTA (extend primer) **(SEQ ID NO: 67)**.

Please delete the paragraph [00183] and replace it with the following amended paragraph:

Oligonucleotide primers were designed based upon the *P. obesus* sequence using Primer Express software (version 1.5), which was obtained at the http address

docs.appliedbiosystems.com/pebiodocs/04303014.pdf. For PCR reactions, forward primers having the sequences GCTGTGTGGCAGTTCCGCAA **(SEQ ID NO: 68)**; GTTCCGCAATATGATCAAGTGC **(SEQ ID NO: 69)**; GATGAAACTCCTTCTGCTGGCTG **(SEQ ID NO: 70)**; and SAAGATGAAACTCCTTCTGCTG **(SEQ ID NO: 71)** were utilized in conjunction with reverse primers having the sequences GGTGAAATAAGACAGCAAGG **(SEQ ID NO: 72)**; GGAGAANCAGATGGCGGCCT **(SEQ ID NO: 73)**; CGGTCACAGTTGCAGATGAAG **(SEQ ID NO: 74)**; GGAAGTGGGGTGACAGCCTAACA **(SEQ ID NO: 75)**; and GGTGACAGSCTAACAGWNTTTC **(SEQ ID NO: 76)**, where S is G or C; N is C, G, T, or A; and W is A or T. Also, another forward primer having the sequence 5'-GCACCCCAGTGGACGAATT-3' **(SEQ ID NO: 77)** and a reverse primer having the sequence 5'-TCAGCCTCTTGGCCTTAGTGTAG-3' **(SEQ ID NO: 78)** yielded an amplicon that was 70 base pairs in length and were used for RT-PCR. Primers for the endogenous control gene, cyclophilin, were designed based on the *P. obesus* sequence. Primer sequence specificity was confirmed by comparing the primer sequences against the GenBank nucleotide sequence for PLA2G1B using BLAST. Primers were synthesized at a 40 nmole concentration and purified by using a reverse-phase cartridge (GeneWorks, Australia).